IN THE SPECIFICATION

Please amend the specification as follows:

Please add the following paragraph on page 1 after the title but before the Field of the Invention·

B1 --This is a Continuation-In-Part of US Application No. 09/323,873, filed June 1, 1999.--

Please delete the following sentence from page 7, line 15:

--FIG. 11. Primary structural comparisons of STEAP proteins:--

Please substitute the following paragraph for the paragraph starting on page 7, line 17:

B2 --Fig. 11A. Amino acid sequence alignment of STEAP-1 (8P1D4 clone 10; SEQ ID NO:2), STEAP-2 (98P4B6 clone GTD3; SEQ ID NO:6), STEAP-3 (98P4B6 clone GTD3; SEQ ID NO:8), and STEAP-4/R80991 (SEQ ID NO:13) using PIMA program (PIMA 1.4 program available at Internet address: http:\\dot.imgen.bcm.tmc.edu:9331\multi-align\multi-align.html); transmembrane domains identified by the SOSUI program (available at Internet address: http:\\www.tuat.ac.jp\~mitaku\adv_sosui\submit.html) are in bold. PIMA maximal linkage clustering results shown; identical residues shown in bold.--

Please substitute the following paragraph for the paragraph starting on page 7, line 23:

B3 --FIG. 11B. Amino acid sequence alignment of STEAP-1 (8P1D4 clone 10; portion of SEQ ID NO:1) and STEAP-2 (98P4B6 clone GTD3; portion of SEQ ID NO:6) sequences. The alignment was performed using the SIM alignment program of the Baylor College of MEdicine Search LAuncher Web site. Transmembrane domains are indicated in boldface. The results show a 54.9% identity in a 237 residues overlap (Score 717.0; Gap frequency:0.0%).--

Please substitute the following paragraph for the paragraph starting on page 7, line 29:

B4 --FIG 11C. Amino acid sequence alignment of STEAP-1 (8P1D4 clone 10; portion of SEQ ID NO:2) and STEAP-3 (98P4B6 clone GTD3; portion of SEQ ID NO:8) sequences. Identical residues indicated with asterisks. SIM results: 40.9% identity in 264 residues overlap; Score 625.0; Gap frequency: 0.0%.--

Please substitute the following paragraph for the paragraph starting on page 7, line 33:

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--FIG 11D. Amino acid sequence alignment of STEAP-2 and STEAP-3 (98P4B6 clone GTD3; portion of SEQ ID NO:8) sequences. Identical residues indicated with asterisks. SIM results: 47.8% identity in 416 residues overlap; Score 1075.0; Gap frequency: 0.2%.--

Please substitute the following paragraph for the paragraph starting on page 7, line 37, spanning pages 8-9:

B6

--FIG. 12. Expression of STEAP-3 mRNA in normal tissues by Northern blot (FIG. 12A) and RT-PCR (FIG. 12B). For RT-PCR analysis, first strand cDNA was prepared from 16 normal tissues. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to AI139607, shows predominant expression of AI139607 in placenta and prostate after 25 cycles of amplification. The following primers were used to amplify AI139607:

AI139607.15' TTAGGACAACTTGATCACCAGCA 3' (SEQ ID NO: 16)
AI139607.25' TGTCCAGTCCAAACTGGGTTATTT 3' (SEQ ID NO: 17)--

Please substitute the following paragraph for the paragraph starting on page 9, line 7:

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--FIG. 13. Predominant expression of STEAP-4/R80991 in liver. First strand cDNA was prepared from 16 normal tissues. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to R80991, shows predominant expression of R80991 in liver after 25 cycles of amplification. The following primers were used to amplify R80991:

R80991.1 5' AGGGAGTTCAGCTTCGTTCAGTC 3' (SEQ ID NO: 18)
R80991.2 5' GGTAGAACTTGTAGCGGCTCTCCT 3' (SEQ ID NO: 19)--

Please substitute the following paragraph for the paragraph starting on page 9, line 14:

B8

--FIG. 14. Predominant expression of STEAP-2 (98P4B6) in prostate tissue. First strand cDNA was prepared from 8 normal tissues, the LAPC xenografts (4AD, 4AI and 9AD) and HeLa cells. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 98P4B6, shows predominant expression of 98P4B6 in normal prostate and the LAPC xenografts. The following primers were used to amplify STEAP II:

98P4B6.1 5' GACTGAGCTGGAACTGGAATTTGT 3' (SEQ ID NO: 20)
98P4B6.2 5' TTTGAGGAGACTTCATCTCACTGG 3' (SEQ ID NO: 21)--

Please substitute the following lines for the lines starting on page 34, lines 10-11:

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--RSACDN (cDNA synthesis primer):

5'TTTT**GTAC**AAGCTT$_{30}$3' (SEQ ID NO: 22)--

Please substitute the following lines for the lines starting on page 34, lines 13-15:

--Adaptor 1:

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5'CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAG**GT**3' (SEQ ID NO: 23)

3'GGCCCGTC**CA**5' (SEQ ID NO: 24)--

Please substitute the following lines for the lines starting on page 34, lines 16-18:

--Adaptor 2:

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5'GTAATACGACTCACTATAGGGCAGCGTGGTCGCGGCCGAG**GT**3' (SEQ ID NO: 25)

3'CGGCTC**CA**5' (SEQ ID NO: 26)--

Please substitute the following lines for the lines starting on page 34, lines 19-20:

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--PCR primer 1:

5'CTAATACGACTCACTATAGGGC3' (SEQ ID NO: 27)--

Please substitute the following lines for the lines starting on page 34, lines 22-23:

B13

--Nested primer (NP)1:

5'TCGAGCGGCCGCCCGGGCAG**GT**3' (SEQ ID NO: 28)--

Please substitute the following lines for the lines starting on page 34, lines 25-26:

B14

--Nested primer (NP)2:

5'AGCGTGGTCGCGGCCGAG**GT**3' (SEQ ID NO: 29)--

Please substitute the following paragraph for the last full paragraph on page 36:

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--To determine expression levels of the 8P1D4 gene, 5 μl of normalized first strand cDNA was analyzed by PCR using 25, 30, and 35 cycles of amplification using the following primer pairs, which were designed with the assistance of (MIT):--

Please substitute the following lines for the lines starting on page 37, lines 2-3:

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--5' ACT TTG TTG ATG ACC AGG ATT GGA 3' (SEQ ID NO: 14)

B16 5' CAG AAC TTC AGC ACA CAC AGG AAC 3' (SEQ ID NO: 15)--

Please substitute the following paragraph for the paragraph starting on page 40, line 9:

--A 15 mer peptide corresponding to amino acid residues 14 through 28 of the STEAP-1 amino acid sequence as shown in FIG. 1A (WKMKPRRNLEEDDYL (portion of SEQ ID NO:2)) was synthesized and used to immunize sheep for the generation of sheep polyclonal antibodies towards the amino-terminus of the protein (anti-STEAP-1) as follows. The peptide was conjugated to KLH (keyhole limpet hemocyanin). The sheep was initially immunized with 400 (g of peptide in complete Freund's adjuvant. The animal was subsequently boosted every two weeks with 200 (g of peptide in incomplete Freund's adjuvant. Anti-STEAP antibody was affinity-purified from sheep serum using STEAP peptide coupled to affi-gel 10 (Bio Rad). Purified antibody is stored in phosphate-buffered saline with 0.1% sodium azide.--

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Please substitute the following paragraph for the paragraph starting on page 41, line 3:

--To determine the extent of STEAP-1 protein expression in clinical materials, tissue sections were prepared from a variety of prostate cancer biopsies and surgical samples for immunohistochemical analysis. Tissues were fixed in 10% formalin, embedded in paraffin, and sectioned according to standard protocol. Formalin-fixed, paraffin-embedded sections of LNCaP cells were used as a positive control. Sections were stained with an anti-STEAP-1 polyclonal antibody directed against a STEAP-1 N-terminal epitope (as described immediately above). LNCaP sections were stained in the presence of an excess amount of the STEAP-1 N-terminal peptide immunogen used to generate the polyclonal antibody (peptide 1) or a non-specific peptide derived from a distinct region of the STEAP-1 protein (peptide 2; YQQVQQNKEDAWIEH (SEQ ID NO: 30)).--

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Please substitute the following paragraph for the second full paragraph on page 44:

--The STEAP-2 cDNA (98P4B6-GTD3) contains a 355 bp 5'UTR (untranslated region) that is 72% GC rich, suggesting that it contains translational regulatory elements. The cDNA encodes an open reading frame (ORF) of 454 amino acids (a.a.) with six potential transmembrane domains. This is in contrast to STEAP, which is 339 a.a. in length. Alignment with STEAP-1 demonstrates 54.9% identity over a 237 amino acid overlap. Interestingly, the

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locations of the six putative transmembrane domains in STEAP-2 coincide with the locations of the transmembrane domains in STEAP-1 (see alignment). The homology of STEAP-2 with STEAP-1 is highest in the regions spanned by the first putative extracellular loop to the fifth transmembrane domain. This analysis and the sequence of STEAP-2 suggest some significant differences between STEAP-1 and STEAP-2: STEAP-2 exhibits a 205 a.a. long intracellular N-terminus (compared to 69 a.a. in STEAP-1) and a short 4 a.a. intracellular C-terminus (compared to 26 a.a. in STEAP-1). These differences could imply significant differences in function and/or interaction with intracellular signaling pathways. To identify a unique mouse EST corresponding to STEAP-2, the unique N-terminus of STEAP-2 was used to query the dbest database. One EST mouse EST was isolated (AI747886), mouse kidney) that may be used in the identification of mouse STEAP-2 and in expression analysis of STEAP-2 in mouse.--

Please substitute the following lines for the lines starting on page 46, lines 20-22:

--The following PCR primers were used for STEAP-1:

8P1D4.1	5' ACTTTGTTGATGACCAGGATTGGA 3'	(SEQ ID NO:14)
8P1D4.2	5' CAGAACTTCAGCACACACAGGAAC 3'	(SEQ ID NO:15)--

Please substitute the following lines for the lines starting on page 46, lines 30-32:

--The following PCR primers were used for 98P4B6/STEAP-2:

98P4B6.1	5' GACTGAGCTGGAACTGGAATTTGT 3'	(SEQ ID NO:20)
98P4B6.2	5' TTTGAGGAGACTTCATCTCACTGG 3'	(SEQ ID NO:21)--

Please substitute the following lines for the lines starting on page 47, lines 1-3:

--The following PCR primers were used for AI139607:

AI139607.1	5' TTAGGACAACTTGATCACCAGCA 3'	(SEQ ID NO:16)
AI139607.2	5'TGTCCAGTCCAAACTGGGTTATTT3'	(SEQ ID NO:17)--

Please substitute the following lines for the lines starting on page 47, lines 10-12:

--The following PCR primers were used for R80991:

R80991.3	5' ACAAGAGCCACCTCTGGGTGAA 3'	(SEQ ID NO:33)
R80991.4	5' AGTTGAGCGAGTTTGCAATGGAC 3'	(SEQ ID NO:34)--

Please Substitute the following two tables for the tables on page 49:

STEAP-1 (SEQ ID NO:2)			
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of Molecule Containing This Subsequence)
1	165	GLLSFFFAV (portion of SEQ ID NO:2)	10776.470
2	86	FLYTLLREV (same)	470.951
3	262	LLLGTIHAL (same)	309.050
4	302	LIFKSILFL (same)	233.719
5	158	MLTRKQFGL (same)	210.633

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STEAP-2 (SEQ ID NO:6)			
Rank	Start Position	Subsequence Residue Listing	Score (Estimate of Half Time of Disassociation of Molecule Containing This Subsequence)
1	227	FLYSFVRDV (portion of SEQ ID NO:6)	1789.612
2	402	ALLISTFHV (same)	1492.586
3	307	LLSFFFAMV (same)	853.681
4	306	GLLSFFFAM (same)	769.748
5	100	SLWDLRHLL (same)	726.962